High Resolution Electron Microscopy



Discussions for a

National Molecular Microscopy Laboratory

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Laboratory of Cell Biology Center for Cancer Research National Cancer Institute

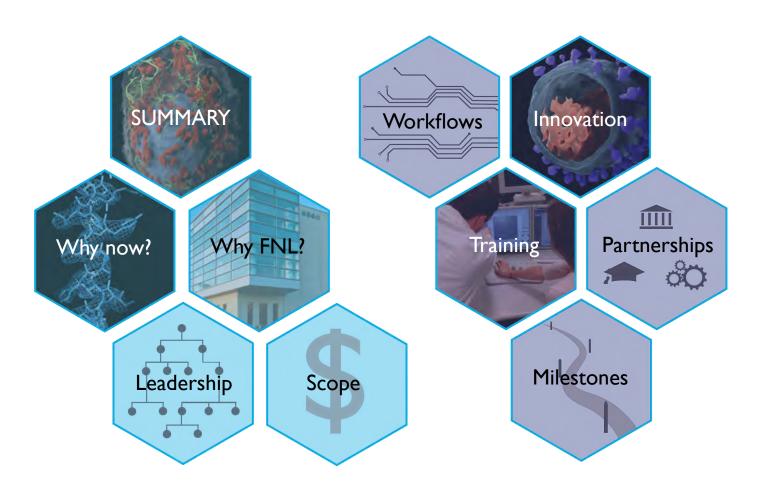
September 2014







Outline of presentation

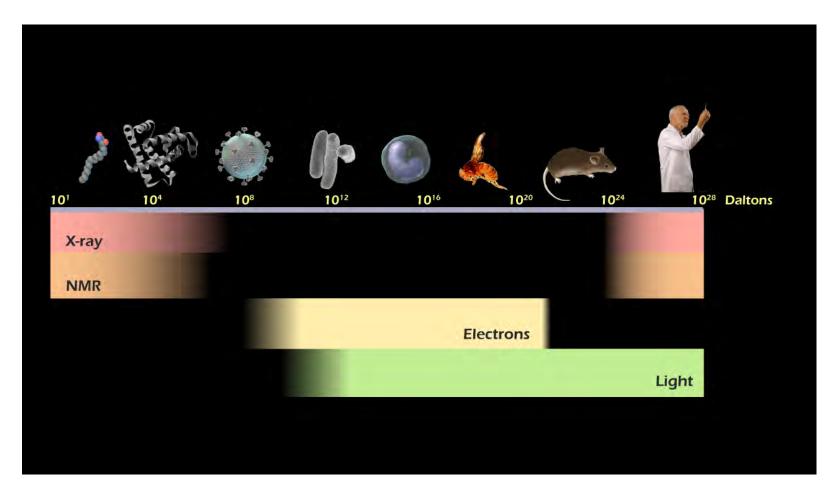








Imaging gaps in biology and medicine



Subramaniam, Curr. Opin. Microbiol. (2005)









2005-2014: A 10-year plan in molecular microscopy

3D mapping of cancer cells

Spatial architecture of signal transduction

Mechanisms of HIV entry

Protein complexes in metabolism

— 15000 nm

— 1500 nm

Mechanisms of HIV entry

Protein complexes in metabolism

— 150 nm

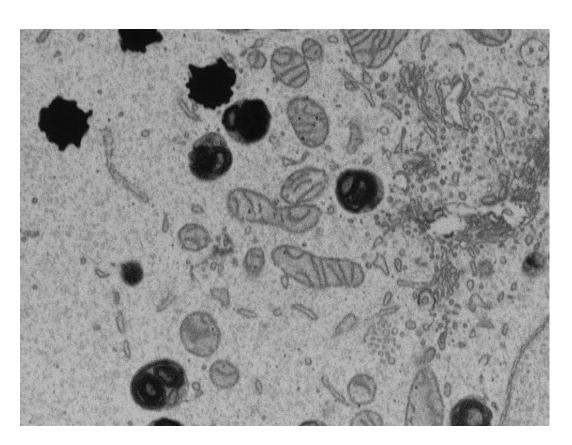
— 15 nm

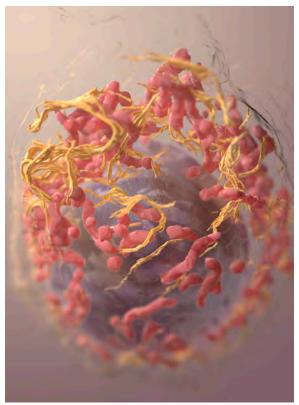












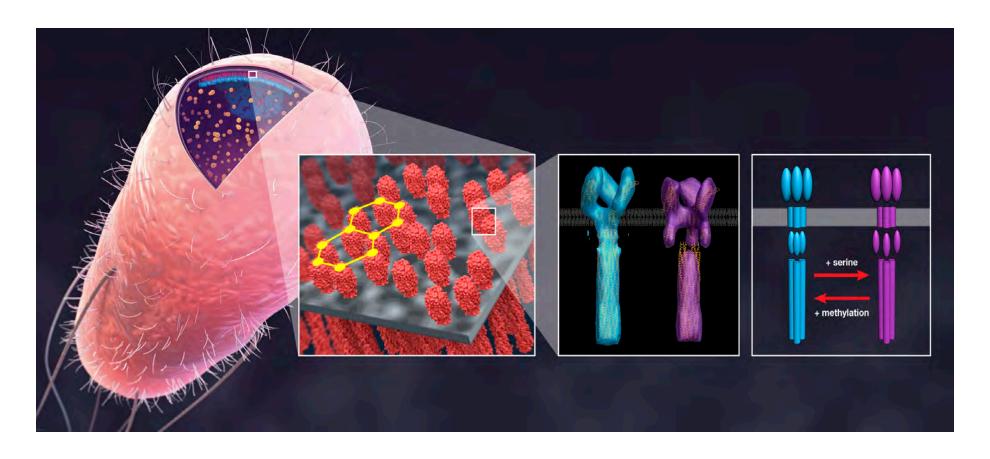








Imaging receptor arrays and signaling complexes in intact cells



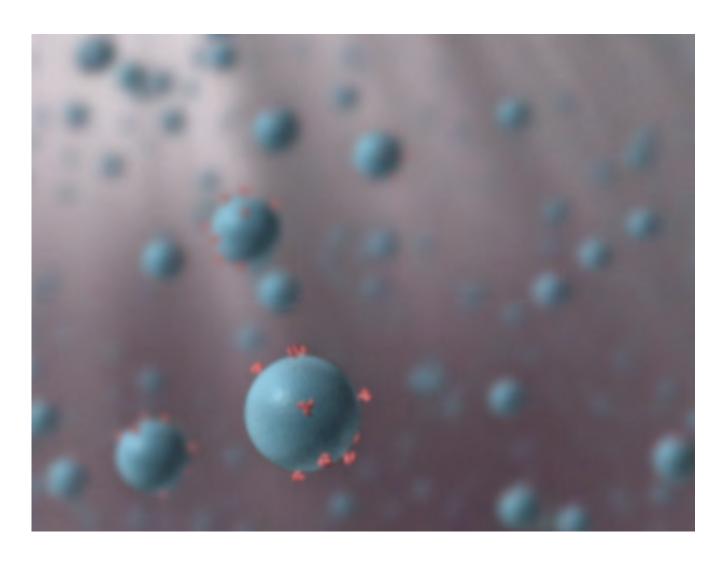








Cryo-electron tomography of HIV



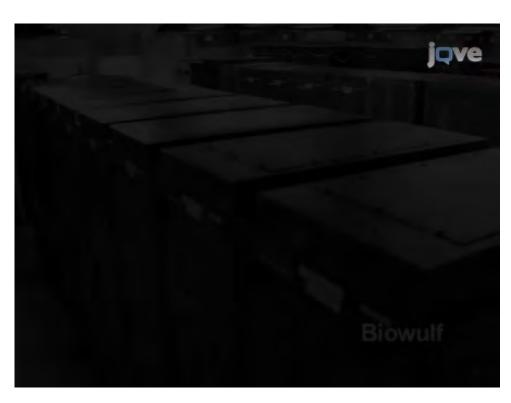








From spikes to structure





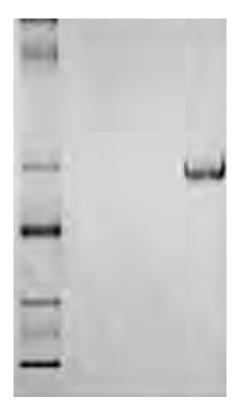








Structure determination without crystallography: A biochemist's dream



Purified protein complex



Vision for a structure determination machine

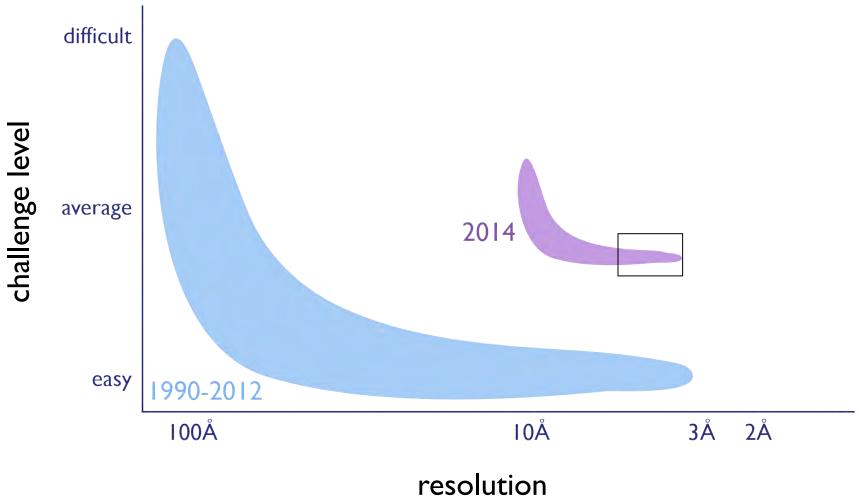








Recent progress in cryo-EM field











The emergence of atomic resolution cryo-EM

Henderson, Quart. Rev. Biophys. (1995)

The potential and limitations of neutrons, electrons and X-rays for atomic resolution microscopy of unstained biological molecules

RICHARD HENDERSON

MRC Laboratory of Molecular Biology, Hills Road, Cambridge CB2 2QH, UK

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1990: First atomic resolution model from electron crystallography of 2D protein crystals (3.5 Å)

1995: Articulation of prospects of obtaining atomic resolution protein structures without crystals

2008: First near-atomic resolution icosahedral viral structures (3.9 Å)

2013: First near-atomic resolution membrane protein structure (3.4 Å)

2014: Structure of a dynamic metabolic enzyme implicated in cancer (3.0 Å)

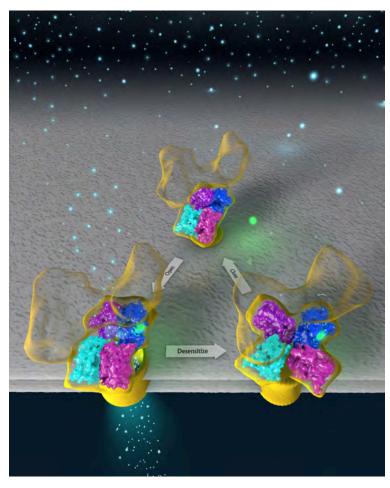


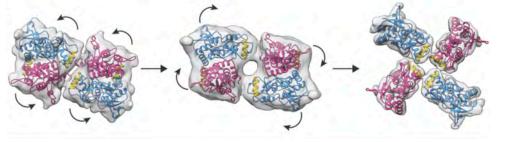




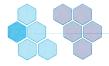


Glutamate receptor gating cycle





Meyerson et al Nature (2014)

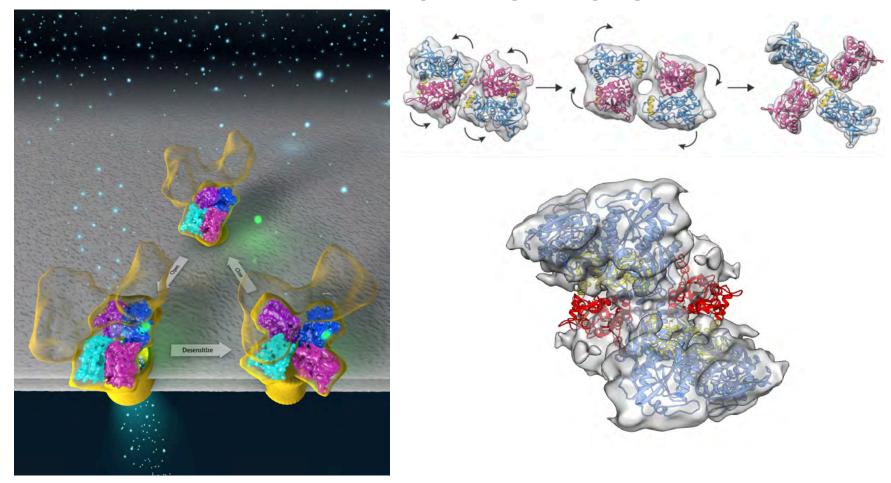








Glutamate receptor gating cycle

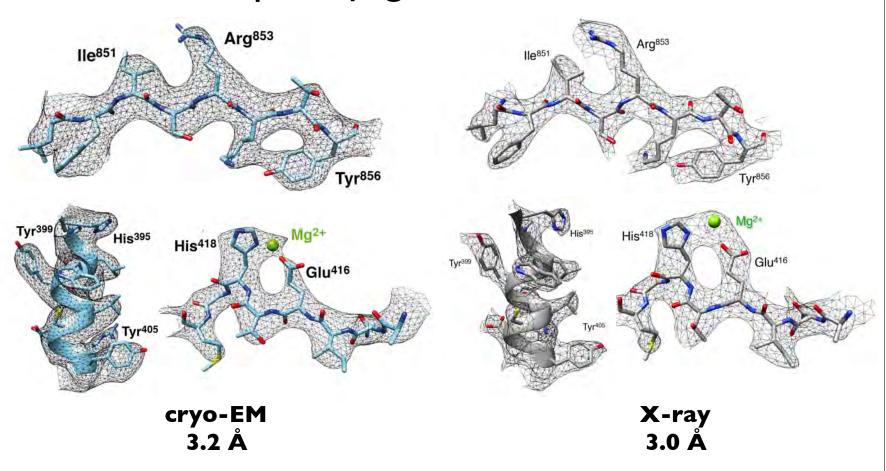


Precise knowledge of protein movements will enable design of drugs that trap distinct functional states





Comparison between cryo-EM and X-ray maps of β -galactosidase





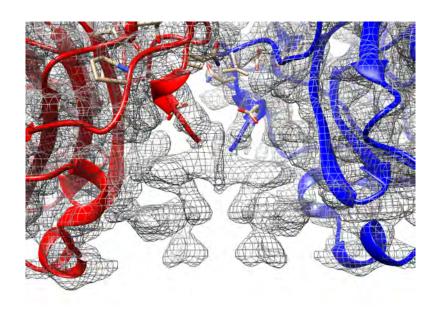
Bartesaghi et al Proc. Natl. Acad. Sci. USA (2014)



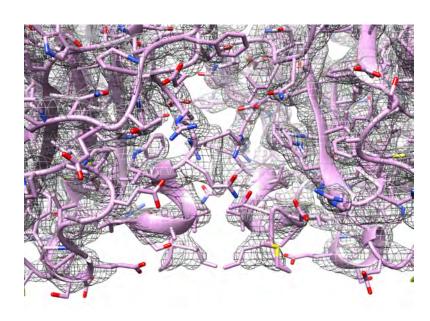




Cryo-EM structure of β -galactosidase at 3.2 Å resolution



Fitted with X-ray coordinates



Fitted with cryo-EM coordinates

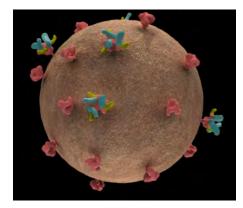
Cryo-EM can provide atomic resolution structures of fulllength proteins under native conditions











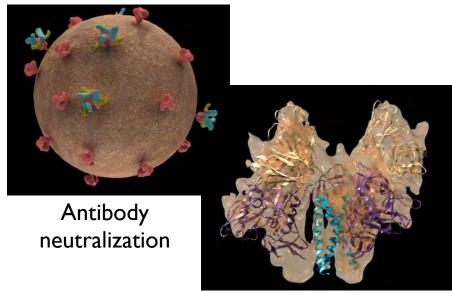
Antibody neutralization











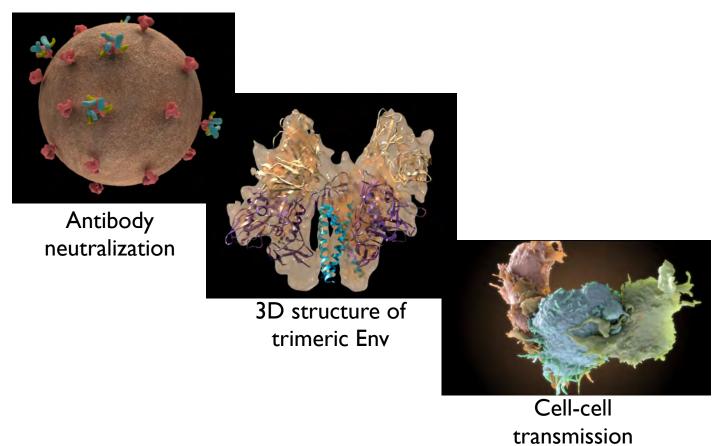
3D structure of trimeric Env









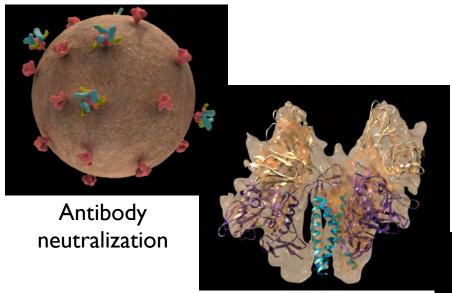








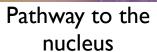




3D structure of trimeric Env

Cell-cell transmission

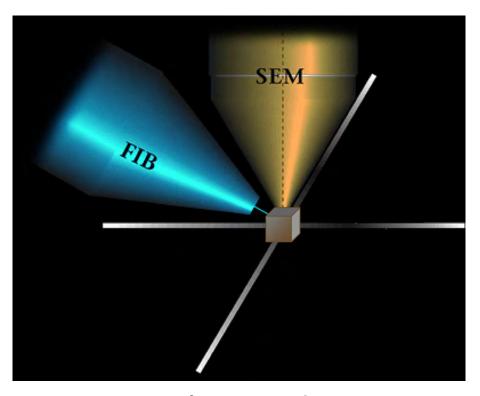
A complete understanding of the problem requires integration of information across cellular and molecular scales

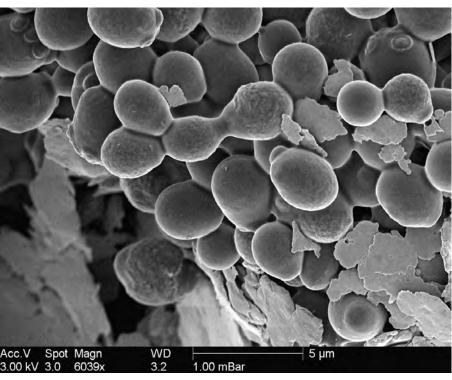












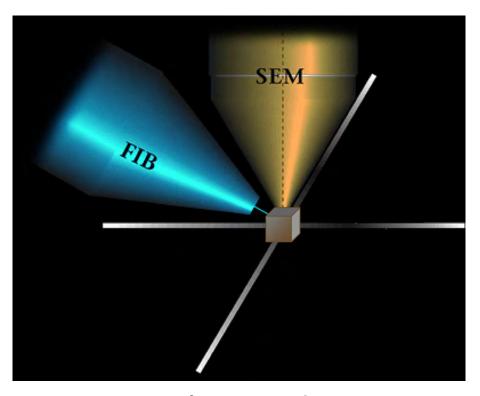
Iteration of slicing and imaging

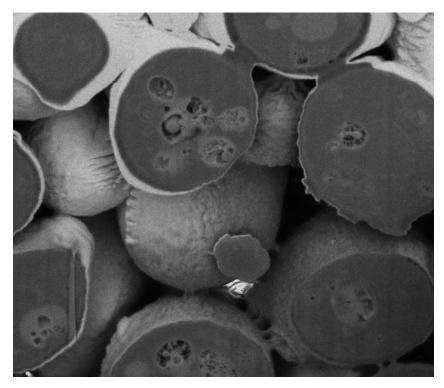












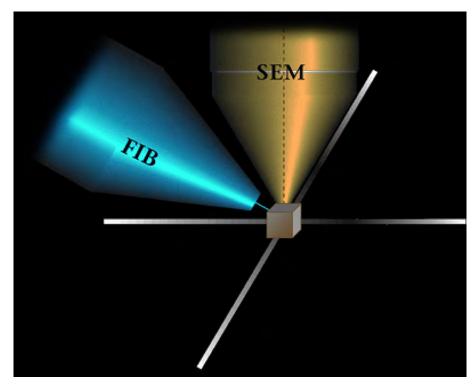
Iteration of slicing and imaging



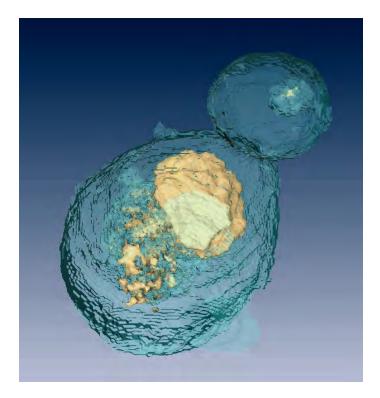








Iteration of slicing and imaging



Heymann et al (2006)

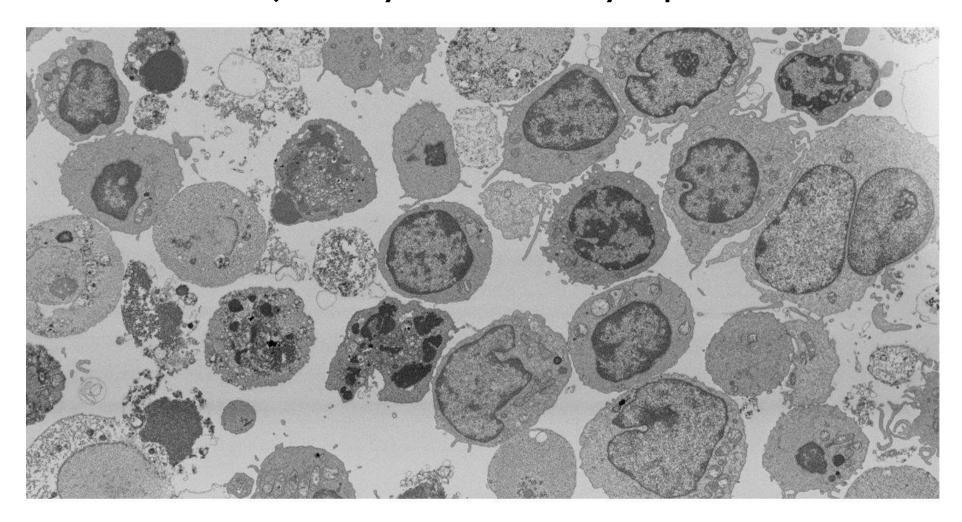








A journey into T-cell synapses



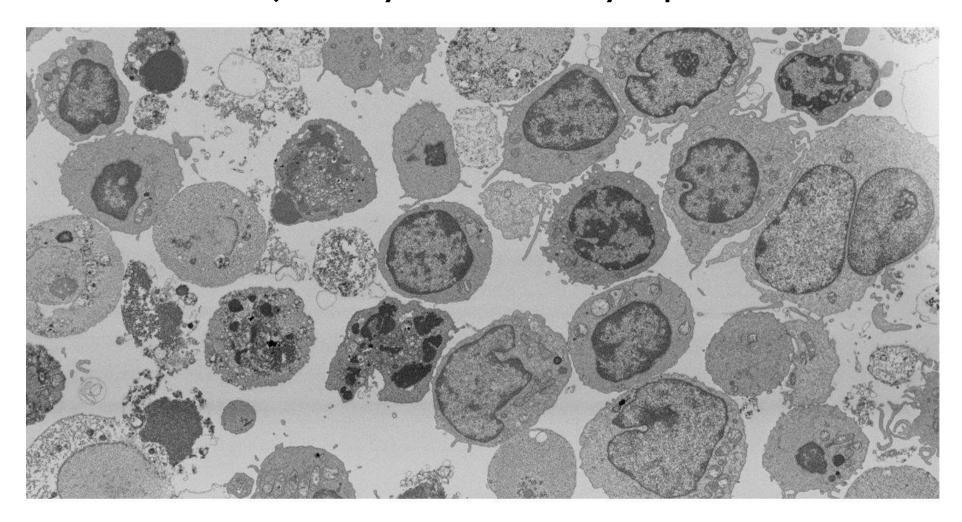








A journey into T-cell synapses



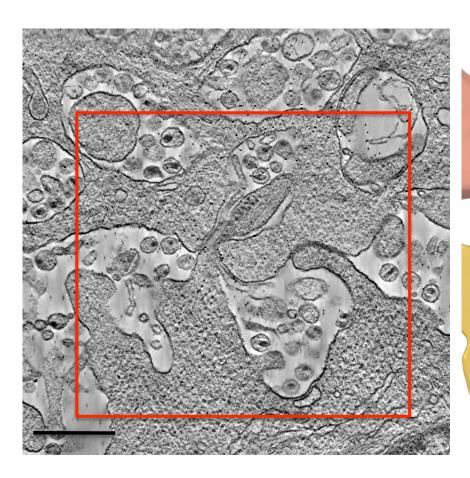


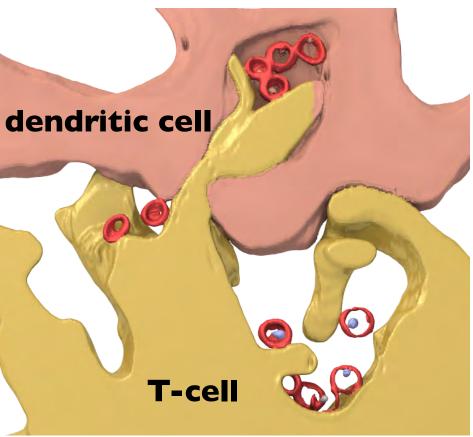






Intimate contact at the cell-cell interface





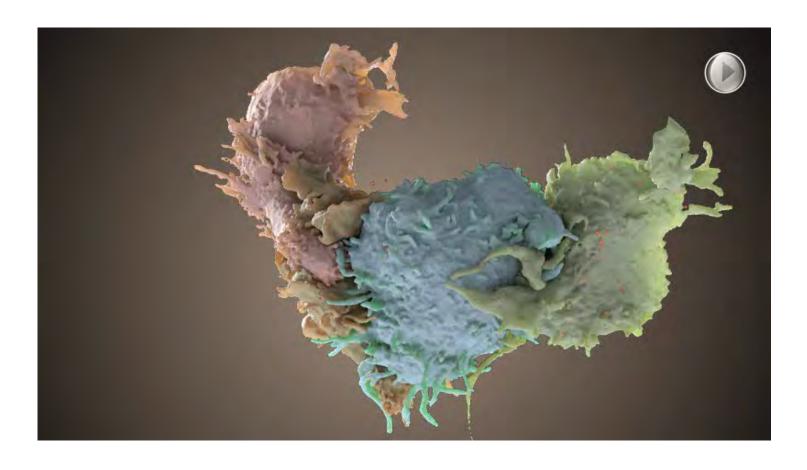








Synapses between primary T-cells



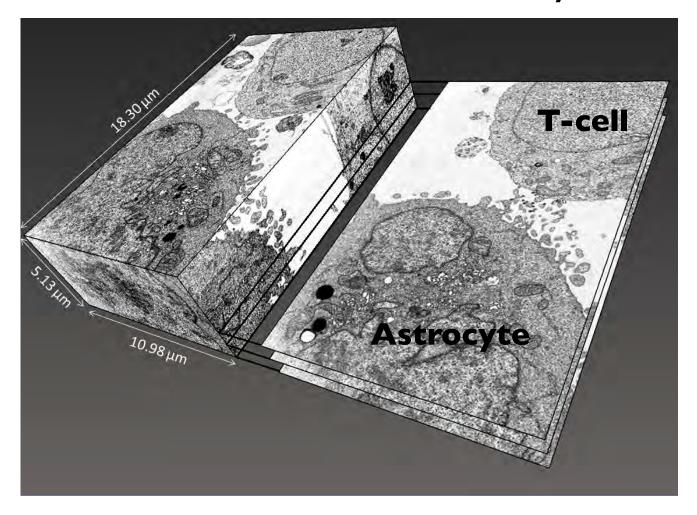






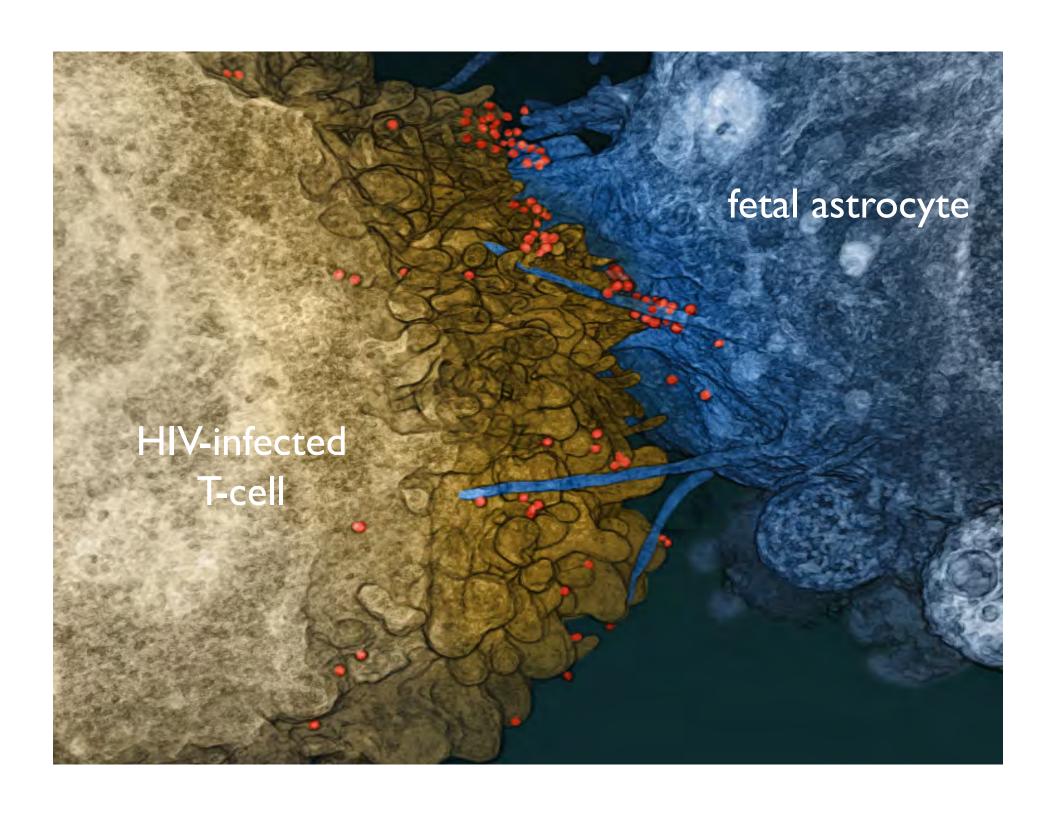


HIV transfer to fetal astrocytes





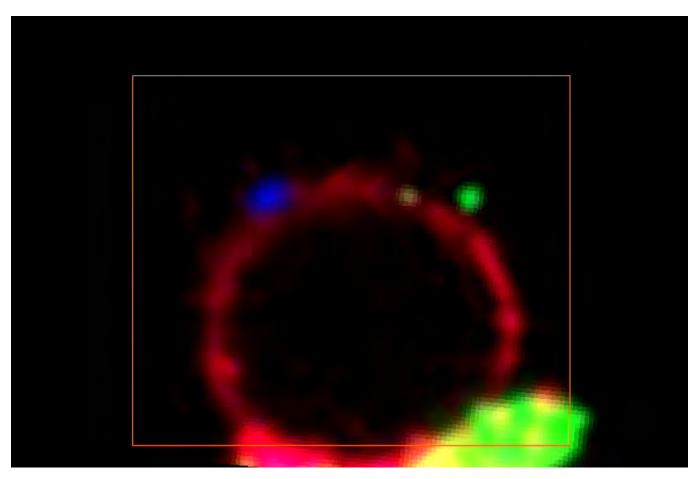








Correlative live confocal and ion-abrasion SEM imaging: A cell biologist's dream





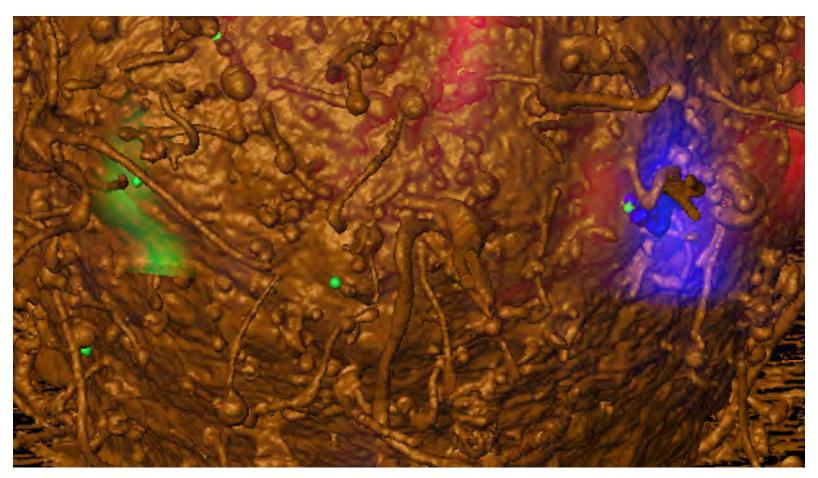


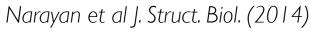






Correlative live confocal and ion-abrasion SEM imaging: A cell biologist's dream





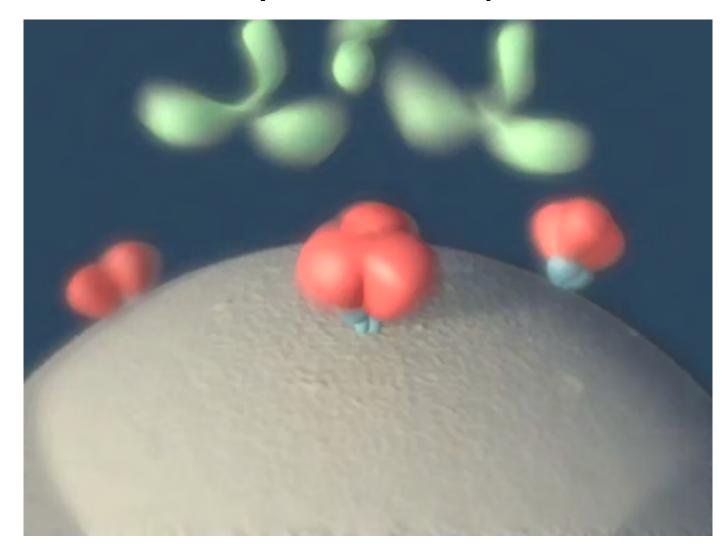








The dynamic HIV spike



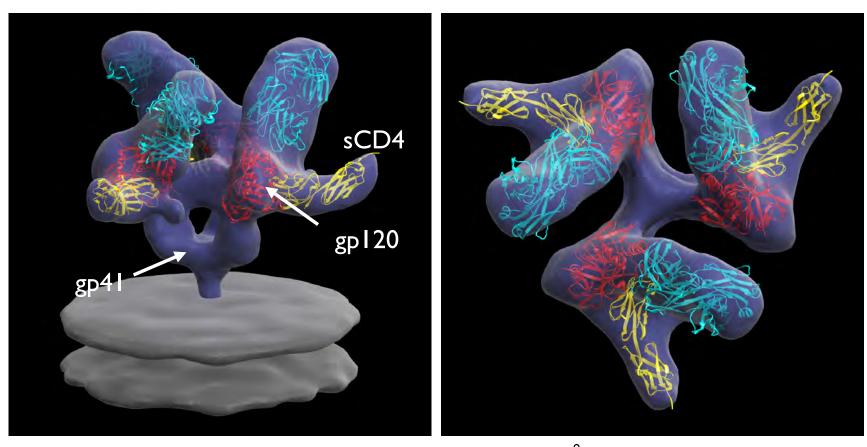








Molecular architecture of trimeric HIV envelope glycoproteins



Subtomogram averages at ~ 20 Å resolution

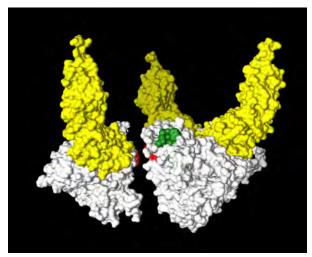




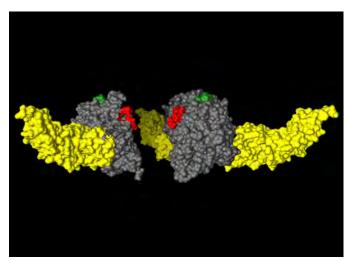




Catching HIV in the act with electron tomography







closed open

Liu et al, Nature (2008)

White et al PLoS Path. (2010)

Tran et al PLos Path. (2012)

Meyerson et al PNAS (2013)

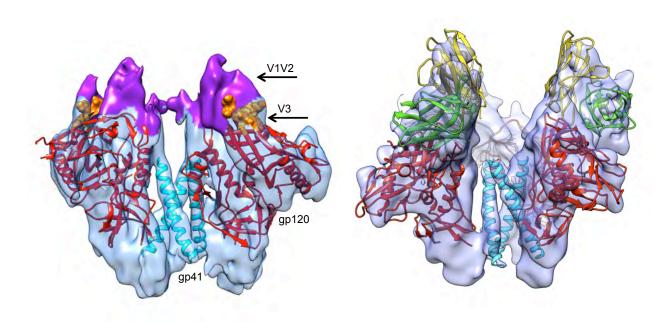


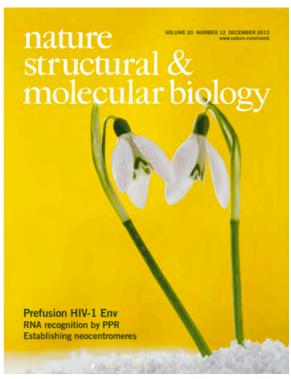






Structures of soluble HIV-1 Env immunogens at ~ 6Å - 9Å resolution





Bartesaghi et al (2013)









Why FNL?

- c-CRADA mechanism for facile collaborations with industrial and academic collaborators
- Strong infrastructure can be established at FNL for collaborations requiring support for pre-microscopy (biochemistry) and post-microscopy (computing) applications
- CCR/NCI cryo-EM program already has footprint at ATRF
- Proximity to many leading institutions along East Coast with strong structural biology programs









Scope

- Similarities and differences with DOE national laboratories that support high resolution electron microscopy
- National laboratory versus local academic user facilities
- Private sector and NIH-wide participation
- Synergy between components that provide user access to existing technologies versus those that develop breakthrough technologies
- Budget considerations









Leadership

- Set clear long-term vision for laboratory
- Important to maintain both technology development and routine user access components of laboratory
- Nucleation of highly motivated multi-disciplinary teams that can identify and tackle difficult challenges
- Effective strategies to stay at forefront of new developments in structural and cell biology
- Opportunity to establish internationally unique center







Training

- Mechanisms to host long-term and short-term visits from extramural researchers
- Core team of specialists to provide support in all aspects of structural investigation from biochemistry to computation
- Resident scholar program
- Strong training partnerships with neighboring institutions
- Peer review and competitive award by extramural study section panel



